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Final Abstract Number: 40.045 Session: Antibiotic Resistance Date: Thursday, April 3, 2014 Time: 12:45-14:15 Room: Ballroom

Presence of virulence gene markers in vibrio strains from an abattoir: Public health implications

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Background: *Vibrio* species are gram-negative bacterium widely distributed in the aquatic environment. Several virulence factors have been associated with pathogenicity of vibrios such as proteases, phospholipases, hemolysins, cysteine proteases, and bacteriocin-like substance. This study evaluates the antibiotic resistance and putative virulence-associated genes of *Vibrio* strains isolated from abattoir effluents in an urban community.

Methods & Materials: The disk diffusion method was used for the characterization of the antibiogram of the isolates. Polymerase chain reaction (PCR) was employed to evaluate the presence of virulence-associated and resistance genes profiles using specific primer sets.

Results: *V. vulnificus, V. metschnikovii, V. fluvialis* and other *Vibrio* sp were isolated from abattoir environment. The *Vibrio* strains showed the typical multidrug-resistance phenotype of an SXT element. The resistance genes detected includes *dfr18* and *dfrA1* for trimethoprim; *floR, tetA, strB, sul2* for chloramphenicol, tetracycline, streptomycin and sulfamethoxazole respectively. Virulence markers of the isolates by PCR revealed the presence of *toxR* (100%), *rtxA* (75.5%), *hlyA* (65.5%), *zot* (43.6%), and *tcpA-acfB* (21.5%) genes. The virulence gene clusters *ctxA*, *ompU* and *ace* were not detected. Comparing the resistance pattern and the virulence profile among the environmental isolates it was observed that cefotaxime, sulphamethoxazole, trimethoprim and nalidixic acid resistant strains have high incidence of *toxR*, *rtxA* and *hlyA* genes.

Conclusion: The findings indicated that the investigated abattoir environments are potential reservoirs for multidrug resistant vibrios strains, and that the non-cholera vibrios pathogens can no longer be ignored as an environmental reservoir of virulence genes.

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New Delhi Metallo- β -lactamase (bla_{NDM-1}) in Gram-negative rods: Causing infections in children



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Background: New Delhi Metallo- β -lactamase-1 (NDM-1) is a type of Metallo- β -lactamase named after the city of origin "New Delhi". The organisms acquiring $bla_{\text{NDM-1}}$ gene are resistant to multiple classes of antibiotics including β -lactams and carbapenems too. This leaves very limited options for the treatment of such infections. NDM-1 producing pathogens can lead to high rate of morbidity and mortality particularly in children. Therefore this study was planned to determine the frequency of $bla_{\text{NDM-1}}$ gene in Gram-negative rods from ≤ 5 years of children.

Methods & Materials: One hundred carbapenems resistant Gram-negative rods were collected from four different children hospitals. The organisms were isolated from different clinical samples (blood, urine, catheter tips, pus). Isolates were reconfirmed to be carbapenems resistant and were identified by colony morphology and biochemical profile using API 20E and 20NE. Antimicrobial susceptibility testing was performed using Kirby-Bauer disc diffusion method according to CLSI 2011. Carbapenems resistant isolates were analyzed for carbapenemases and MBL production according to CLSI 2011 guidelines. MBL producing microbes were further identified for *bla*_{NDM-1} gene using nested PCR.

Results: Out of 100 carbapenems resistant isolates more than 90% showed resistance against commonly used antibiotics including carbapenems. Polymixin B was the only drug which showed 71% susceptibility. Eighty-nine isolates were carbapenamase and MBL producers and among these 32(36%) were bla_{NDM-1} gene producers. Major isolates contained bla_{NDM-1} genes were *Klebsiella pneumoniae* (n = 12) followed by *Enterobacter cloacae* (n = 10) and *Pseudomonas aeruginosa* (n = 6). Most effective drug against bla_{NDM-1} producing bugs was also Polymixin B. bla_{NDM-1} positive isolates were predominantly isolated from neonatal septicemia (n = 21) and male to female ratio was 2:1.

Conclusion: The spread of *bla*_{NDM-1} gene among Gram-negative rods is an alarming threat particularly in hospitalized neonates. A national multicenter survey should be carried out to combat this serious problem.

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